



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/932451

Source: OIPE

Date Processed by STIC: 08/27/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-

compliant in Computer Readable form.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 9/932451

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1      Wrapped Aminos
- 2      Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 3      Numbering
- 4      Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 6      "bug"
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 7      (OLD RULES)
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 8      (NEW RULES)
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
Response      scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
is Artificial Sequence
- 11 ✓ Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
"Unknown." Please explain source of genetic material in <220> to <223> section

Using a word processor to create a sequence listing file is not recommended. Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 08/27/2001

PATENT APPLICATION: US/09/932,451

TIME: 13:14:40

Input Set : A:\0800-0026.txt

Output Set: N:\CRF3\08272001\I932451.raw

```

3 <110> APPLICANT: OZAWA, Keiya
4     SHIMPO, Masahisa
5     IKEDA, Uichi
6     MAEDA, Yoshikazu
7     SHIMADA, Kazuyuki
9 <120> TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC
10    FACTORS
12 <130> FILE REFERENCE: 0800-0026
14 <140> CURRENT APPLICATION NUMBER: US/09/932,451
15 <141> CURRENT FILING DATE: 2001-08-17
17 <150> PRIOR APPLICATION NUMBER: 60/226,056
18 <151> PRIOR FILING DATE: 2000-08-17
20 <160> NUMBER OF SEQ ID NOS: 2
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 576
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: VEGF-165
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(576)
36 <400> SEQUENCE: 1
37 atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt gcc ttg ctg ctc      48
38 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
39   1               5               10              15
41 tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga      96
42 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
43   20              25              30
45 gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat qtc tat caq     144
46 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
47   35              40              45
49 cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag     192
50 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
51   50              55              60
53 tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccc ctg     240
54 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
55  65              70              75              80
57 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    288
58 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    336
59 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    384
60 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    432
61 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    480
62 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    528
63 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    576
64 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc    624
65 caa ggc caq cac ata gga gag atg agc ttc cta caq cac aac aaa tgt     672
66 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys

```

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```

67          115          120          125
69 gaa tgc aga cca aag aaa gat aga gca aga caa gaa aat ccc tgt ggg 432
70 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
71      130          135          140
73 cct tgc tca gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg 480
74 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
75 145          150          155          160
77 tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag 528
78 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
79          165          170          175
81 ctt gag tta aac gaa cgt act tgc aga tgt gac aag ccg agg cgg tga 576
82 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
83      180          185          190

```

86 &lt;210&gt; SEQ ID NO: 2

87 &lt;211&gt; LENGTH: 191

88 &lt;212&gt; TYPE: PRT

89 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 91 &lt;220&gt; FEATURE:

W--&gt; 91 &lt;223&gt; OTHER INFORMATION:

91 &lt;400&gt; SEQUENCE: 2

```

92 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
93 1          5          10          15
95 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
96          20          25          30
98 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
99      35          40          45
101 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
102      50          55          60
104 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
105 65          70          75          80
107 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
108          85          90          95
110 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
111          100          105          110
113 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
114          115          120          125
116 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
117      130          135          140
119 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
120 145          150          155          160
122 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
123          165          170          175
125 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
126      180          185          190

```

A Field 213 response of "Artificial Sequence" requires a mandatory explanation or description in field 223.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/932,451

DATE: 08/27/2001

TIME: 13:14:41

Input Set : A:\0800-0026.txt

Output Set: N:\CRF3\08272001\I932451.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:91 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:91 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: